

"A" = filed on 3/27/2002

10/089147

JC13 Rec'd PCT/PTO 27 MAR 2002

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1. An isolated nucleic acid sequence which encodes a polypeptide and which is composed of a combination of the nucleic acid sequences of a biosynthesis nucleic acid sequence of the fatty acid or lipid metabolism and one of the following nucleic acids:
 - a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 1,
 - b) nucleic acid sequences which are derived from the nucleic acid sequence shown in SEQ ID NO: 1 as the result of the degeneracy of the genetic code,
 - c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 1 which encode polypeptides with the amino acid sequences shown in SEQ ID NO: 2 and which have at least 60% homology at the amino acid level,
 - d) a nucleic acid sequence with the sequence shown in SEQ ID NO: 3 or the amino-terminal portion of the coding region of this sequence.
2. An isolated nucleic acid sequence as claimed in claim 1, wherein a sequence of the following protein groups is used as biosynthesis gene nucleic acid sequence of the fatty acid or lipid metabolism:

Acyl-CoA dehydrogenase(s), Acyl-ACP [= acyl carrier protein] desaturase(s), Acyl-ACP thioesterase(s), fatty acid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases and/or fatty acid elongase(s).
3. An isolated nucleic acid sequence as claimed in claim 1, wherein a sequence of

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the following protein groups is used as biosynthesis gene nucleic acid sequence of the fatty acid or lipid metabolism:

fatty acid acyltransferase(s), $\Delta 4$ desaturase, $\Delta 5$ desaturase, $\Delta 6$ desaturase, $\Delta 9$ desaturase, $\Delta 12$ desaturase, $\Delta 15$ desaturase or a fatty acid elongase.

4. An isolated nucleic acid sequence as claimed in claim 1, wherein the derivatives mentioned under (c) have a homology at the amino acid level of 70%, preferably 80%, especially preferably of 90%, over the entire region of the sequence shown in SEQ ID NO: 2 (Program PileUp, J. Mol. Evolution., 25, 351-360, 1987, Higgins et al., CABIOS, 5 1989: 151-153).
5. An amino acid sequence encoded by a nucleic acid sequence as claimed in claim 1.
6. A nucleic acid construct comprising a nucleic acid sequence as claimed in claim 1, wherein the nucleic acid sequence is linked to one or more regulatory signals.
7. The use of a nucleic acid sequence as claimed in claim 1 or of a nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals for the generation of transgenic plants.
8. A vector comprising a nucleic acid sequence as claimed in claim 1 or a nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals.
9. A vector as claimed in claim 8, which is a linear or circular DNA, a phage, a virus,

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- a transposon, an IS element, a phasmid, a phagemid, a cosmid or a plasmid.
10. An organism comprising at least one nucleic acid sequence as claimed in claim 1, at least one nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals or at least one vector comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals or a nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals.
 11. An organism as claimed in claim 10, which is a eukaryotic organism.
 12. An organism as claimed in claim 10, which is a plant, a eukaryotic microorganism or an animal.
 13. An organism as claimed in claim 10, which is a plant, a fungus or a yeast.
 14. An organism as claimed in claim 10, which is *Yarrowia lypolytica*, *Saccharomyces cerevisiae*, *Traustochytrium*, *Arabidopsis thaliana*, *Brassica napus* or *Linum usitatissimum*.
 15. A transgenic plant comprising a nucleic acid sequence as claimed in claim 1 or a nucleic acid construct comprising said nucleic acid sequence.
 16. A method of targeting proteins involved in lipid or fatty acid biosynthesis into liposomes or lipid bodies, which comprises combining the protein-encoding nucleic acids and one of the following sequences to give a joint protein-encoding sequence:
 - a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 1,

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- b) nucleic acid sequences which are derived from the nucleic acid sequence shown in SEQ ID NO: 1 as the result of the degeneracy of the genetic code,
 - c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 1 which encode polypeptides with the amino acid sequences shown in SEQ ID NO: 2 and which have at least 60% homology at the amino acid level,
 - d) a nucleic acid sequence with the sequence shown in SEQ ID NO: 3 or the amino-terminal portion of the coding region of this sequence, and introducing the resulting sequence into a eukaryotic organism.
17. A method of targeting proteins involved in lipid or fatty acid biosynthesis into liposomes or lipid bodies, which comprises introducing at least one nucleic acid sequence as claimed in claim 1 or at least one nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals into an oil-producing organism.
18. A method of producing fatty acids or lipids, which comprises introducing at least one nucleic acid sequence as claimed in claim 1 or at least one nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals into an oil-producing organism, growing this organism and isolating the oil contained in the organism.
19. A method of producing fatty acids, which comprises introducing at least one nucleic acid sequence as claimed in claim 1 or at least one nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals into an oil-producing organism, growing this

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organism, isolating the oil contained in the organism and liberating the fatty acids.

20. A method as claimed in claim 16, wherein the organism is a plant or a eukaryotic microorganism.

"B" = filed on 5/14/2009

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COMPLETE LISTING OF ALL CLAIMS IN THE APPLICATION

1. (original) A nucleotide sequence encoding a plant s-adenosylmethionine:Mg-protoporphyrin IX O-methyltransferase or parts, derivatives homologs or isoforms thereof.
2. (original) A nucleotide sequence as claimed in claim 1, which comprises the coding sequence as shown in SEQ ID NO 1.
3. (original) A nucleotide sequence as claimed in claim 1, which comprises the coding sequence as shown in SEQ ID NO 2 and/or SEQ ID NO 3.
4. (original) A nucleotide sequence as claimed in claim 1, which comprises the coding sequence as shown in SEQ ID NO 4.
5. (original) A nucleotide sequence as claimed in claim 1, wherein the plant protein encoded by it comprises an amino acid sequence as shown in SEQ ID NO 5.
6. (original) A nucleotide sequence as claimed in claim 1, wherein the plant protein encoded by it comprises an amino acid sequence as shown in SEQ ID NO 6 an/or SEQ ID NO 7.
7. (previously presented) A nucleotide sequence as claimed in claim 1, which encodes a *Physcomitrella patens* amino acid sequence.
8. (previously presented) A nucleotide sequence as claimed in claim 1, which encodes a tobacco amino acid sequence.
9. (previously presented) A nucleotide sequence as claimed in claim 1, which encodes a modified S-adenosylmethionine:Mg-protoporphyrin IX O-methyltransferase or

parts, derivatives, homologs or isoforms thereof tolerating herbicidally active compounds.

10. (previously presented) A gene structure comprising a nucleotide sequence as claimed in claim 1 or parts thereof, and regulatory nucleotide sequences operably linked thereto.
11. (original) A gene structure as claimed in claim 10 comprising regulatory nucleotide sequences from the group of the promoters, enhancers, operators, terminators, polyadenylation signals, targeting sequences, retention signals or translation enhancers.
12. (previously presented) A gene structure as claimed in claim 10 comprising, as regulatory nucleotide sequence, a constitutive promoter.
13. (previously presented) A gene structure as claimed in claim 10 comprising, as regulatory nucleotide sequence a leaf- and/or seed-specific and/or an inducible, preferably light-inducible, promoter.
14. (previously presented) A vector comprising at least one nucleotide sequence as claimed in claim 1 or a gene structure comprising a nucleotide sequence as claimed in claim 1 or parts thereof, and regulatory nucleotide sequences operably linked thereto.
15. (original) A vector as claimed in claim 14 comprising additional nucleotide sequences for the selection and/or replication in a host cell and/or for integration into the host cell.

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16-29. (non-elected)

30-31. (canceled)

"C" = filed on 8/2/2009

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COMPLETE LISTING OF ALL CLAIMS IN THE APPLICATION

1. (original) An isolated nucleic acid sequence which encodes a polypeptide and which is composed of a combination of the nucleic acid sequences of a biosynthesis nucleic acid sequence of the fatty acid or lipid metabolism and one of the following nucleic acids:
 - a. a nucleic acid sequence with the sequence shown in SEQ ID NO: 1,
 - b. nucleic acid sequences which are derived from the nucleic acid sequence shown in SEQ ID NO: 1 as the result of the degeneracy of the genetic code,
 - c. derivatives of the nucleic acid sequence shown in SEQ ID NO: 1 which encode polypeptides with the amino acid sequences shown in SEQ ID NO: 2 and which have at least 60% homology at the amino acid level,
 - d. a nucleic acid sequence with the sequence shown in SEQ ID NO: 3 or the amino-terminal portion of the coding region of the sequence.

2. (original) An isolated nucleic acid sequence as claimed in claim 1, wherein a sequence of the following protein groups is used as biosynthesis gene nucleic acid sequence of the fatty acid or lipid metabolism.

Acyl-CoA dehydrogenase(s), Acyl-ACP[=acyl carrier protein] desaturase(s), Acyl-ACP thioesterase(s), fatty acid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A

oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases and/or fatty acid elongase(s).

3. (previously presented) An isolated nucleic acid sequence as claimed in claim 1, wherein a sequence of the following protein groups is used as biosynthesis gene nucleic acid sequence of the fatty acid or lipid metabolism:
fatty acid acryltransferase(s), $\Delta 4$ desaturase, $\Delta 5$ desaturase, $\Delta 6$ desaturase, $\Delta 9$ desaturase, $\Delta 12$ desaturase, $\Delta 15$ desaturase or a fatty acid elongase.
4. (previously presented) An isolated nucleic acid sequence as claimed in claim 1, wherein the derivatives mentioned under (c) have a homology at the amino acid level of 70%, preferably 80%, especially preferably of 90%, over the entire region of the sequence shown in SEQ ID NO: 2 (Program Pilelp, J. Mol. Evolution., 25, 351-360, 1987, Higgins et al., CABIOS, 5 1989: 151-153).
5. (original) An amino acid sequence encoded by a nucleic acid sequence as claimed in claim 1.
6. (original) A nucleic acid construct comprising a nucleic acid sequence as claimed in claim 1, wherein the nucleic acid sequence is linked to one or more

regulatory signals.

7. (previously presented) The use if a nucleic acid sequence as claimed in claim 1 or of a nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals for the generation of transgenic plants.
8. (previously presented) A vector comprising a nucleic acid sequence as claimed in claim 1 or a nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals.
9. (original) A vector as claimed in claim 8, which is a linear or circular DNA, a phage, a virus, a transposon, a IS element, a phasmid, a phagemid, a cosmid or a plasmid.
10. (previously presented) An organism comprising at least one nucleic acid sequence as claimed in claim 1, at least one nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals or at least one vector comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals or a nucleic acid construct comprising said nucleic acid sequence

wherein the nucleic acid sequence is linked to one or more regulatory signals.

11. (original) An organism as claimed in claim 10, which is a eukaryotic organism.
12. (previously presented) An organism as claimed in claim 10, which is a plant, a eukaryotic microorganism or an animal.
13. (previously presented) An organism as claimed in claim 10, which is a plant, a fungus or a yeast.
14. (previously presented) An organism as claimed in claim 10, which is *Yarrowia lipolytica*, *Saccharomyces cerevisiae*, *Traustochytrium*, *Arabidopsis thaliana*, *Brassica napus* or *Linum usitatissimum*.
15. (previously presented) A transgenic plant comprising a nucleic acid sequence as claimed in claim 1 or a nucleic acid construct comprising said nucleic acid sequence.
16. (previously presented) A method of targeting proteins involved in lipid or fatty acid biosynthesis into liposomes or lipid bodies, which comprises combining the protein-encoding nucleic acids and one of the following sequences to give a joint

protein-encoding sequence:

- a. a nucleic acid sequence with the sequence shown in SEQ ID NO: 1,
 - b. nucleic acid sequences which are derived from the nucleic acid sequence shown in SEQ ID NO: 1 as the result of the degeneracy of the generic code,
 - c. derivatives of the nucleic acid sequence shown in SEQ ID NO: 1 which encode polypeptides with the amino acid sequences shown in SEQ ID NO: 2 and which have at least 60% homology at the amino acid level,
 - d. a nucleic acid sequence with the sequence shown in SEQ ID NO: 3 or the amino-terminal portion of the coding region of this sequence, and introducing the resulting sequence into a eukaryotic organism.
17. (previously presented) A method of targeting proteins involved in lipid or fatty acid biosynthesis into liposomes or lipid bodies, which comprises introducing at least one nucleic acid sequence as claimed in claim 1 or at least one nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals into an oil-producing organism.
18. (previously presented) A method of producing fatty acids or lipids, which comprises introducing at least one nucleic acid sequence as claimed in claim 1 or at least one nucleic acid construct comprising said nucleic acid sequence

wherein the nucleic acid sequence is linked to one or more regulatory signals into an oil-producing organism, growing this organism and isolating the oil contained in the organism.

19. (previously presented) A method of producing fatty acids, which comprises introducing at least one nucleic acid sequence as claimed in claim 1 or at least one nucleic acid construct comprising said nucleic acid sequence wherein the nucleic acid sequence is linked to one or more regulatory signals into an oil-producing organism, growing this organism, isolating the oil contained in the organism and liberating the fatty acids.
20. (previously presented) A method as claimed in claim 16, wherein the organism is a plant or a eukaryotic microorganism.